



SEQUENCE LISTING

<110> Lindquist, et al.

<120> RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS AND METHODS COMPRISING SAME

<130> 30554/34978A

<150> US 09/591,632

<151> 2000-06-09

<150> US 60/138,833

<151> 1999-06-09

<160> 70

<170> PatentIn version 3.3

<210> 1

<211> 3321

<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> CDS

<222> (739) .. (2796)

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attggagttt gaagaaaatc ccaaccctac ggtagaaaat tgaatatcgt atctgtttat 180

acacacatac atacatttata ttataata agcgttaaaa tttcggcaga atatctgtca 240

accacacaaa aatcatacaa cgaatggat atgcttcatt tctttgttgc gcattagctg 300

cgctatttga ctcaaattat tatttttac taagacgacg cgtcacagtgc ttgcagtctg 360

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ttcttccgca aaaagatgaa tcttagttct cagccccacca aaagaggtac atgctaagat 480

catacagaag ttattgtcac ttcttacatt gctcttaaat gtacattaca accgggtatt 540

atatcttaca tcattgtata atatgatctt tctttatgga gaaaattttt ttttactcg 600

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Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln		
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Asn Lys Glu Glu Arg Asn Asp Gly Lys Thr Ile Glu Val Gly Lys Ala	
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Tyr Phe Glu Thr Glu Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly	
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cat aaa atg tac gtt tcc gag atg atc ggt ggt gct tct caa gct gat	1827
His Lys Met Tyr Val Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp	
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Val Gly Val Leu Val Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly	
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Phe Glu Arg Gly Gly Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr	
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Thr Val Asn Trp Ser Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val	
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Phe Met Pro Val Ser Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val	
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Asp Pro Lys Glu Cys Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr	
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Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
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Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
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115 120 125

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
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Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
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Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
195 200 205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
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His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225 230 235 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Met Phe Gly

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255

Gly Lys Asp His Val Ser Leu Ile Phe Met Gly His Val Asp Ala Gly
260 265 270

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275 280 285

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290 295 300

Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
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Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Val Leu Val
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370 375 380

Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
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Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val Phe Met Pro Val Ser
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Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val Asp Pro Lys Glu Cys
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His Val Asp Arg His Ile Asn Ala Pro Phe Met Leu Pro Ile Ala Ala
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Lys Ser Val Thr Lys Phe Val Ala Gln Ile Ala Ile Val Glu Leu Lys
580 585 590

Ser Ile Ile Ala Ala Gly Phe Ser Cys Val Met His Val His Thr Ala
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Ile Glu Glu Val His Ile Val Lys Leu Leu His Lys Leu Glu Lys Gly
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Thr Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met
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Lys Val Ile Ala Val Leu Glu Thr Glu Ala Pro Val Cys Val Glu Thr
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cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr 65 70 75 80	421
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gtg gag tat tcc aga att aca aaa ttt ttt caa gaa caa cca ctg gag Val Glu Tyr Ser Arg Ile Thr Lys Phe Phe Gln Glu Gln Pro Leu Glu 100 105 110	517
gga tat acc ctt ttc tct cac agg tct gcg cct aat gga ttc aaa gtt Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val 115 120 125	565
gct ata gta cta agt gaa ctt gga ttt cat tat aac aca atc ttc cta Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu 130 135 140	613
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90

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Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
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Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
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Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
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Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
180 185 190

Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
195 200 205

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Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
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Gly Val Val Glu Met Ala Leu Ala Glu Arg Arg Glu Ala Leu Val Met
260 265 270

Glu Leu Asp Thr Glu Asn Ala Ala Tyr Ser Ala Gly Thr Thr Pro
275 280 285

Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
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Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val
305 310 315 320

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catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tattttttc	300
aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaagggtga taccttagtt	360
aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa	420
ttggaataaca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatgg	480
atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac	540
cattatcaac aaaatactcc aattggtgat ggtccagtct ttttaccaga caaccattac	600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggcttg	660
ttagaatttg ttactgctgc tggattacc catggatgg atgaattgta caaataa	717
<210> 13	
<211> 27	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> HA tag-encoding sequence	
<400> 13	
tacccataacg acgtcccaga ctacgct	27
<210> 14	
<211> 645	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Yeast Sup35Rdelta2-5 encoding sequence	
<220>	
<221> CDS	
<222> (1)..(645)	
<400> 14	
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac	48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr	
1 5 10 15	
agc cag aac ggt aac caa caa ggt aac aac aga tac caa ggt tat	96
Ser Gln Asn Gly Asn Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr	
20 25 30	
caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat	144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn	
35 40 45	
tac caa ggt tat tct ggg tac cca caa ggt ggc cgt gga aat tac aaa	192
Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys	
50 55 60	
aac ttc aac tac aat aac aat ttg caa gga tat caa gct ggt ttc caa	240
Asn Phe Asn Tyr Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln	

65	70	75	80	
cca cag tct caa ggt atg tct ttg aac gac ttt caa aag caa caa aag				288
Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys				
85	90	95		
cag gcc gct ccc aaa cca aag aag act ttg aag ctt gtc tcc agt tcc				336
Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser				
100	105	110		
ggt atc aag ttg gcc aat gct acc aag aag gtt ggc aca aaa cct gcc				384
Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala				
115	120	125		
gaa tct gat aag aaa gag gaa gag aag tct gct gaa acc aaa gaa cca				432
Glu Ser Asp Lys Lys Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro				
130	135	140		
act aaa gag cca aca aag gtc gaa gaa cca gtt aaa aag gag gag aaa				480
Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys				
145	150	155	160	
cca gtc cag act gaa gaa aag acg gag gaa aaa tcg gaa ctt cca aag				528
Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys				
165	170	175		
gta gaa gac ctt aaa atc tct gaa tca aca cat aat acc aac aat gcc				576
Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala				
180	185	190		
aat gtt acc agt gct gat gcc ttg atc aag gaa cag gaa gaa gaa gtg				624
Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val				
195	200	205		
gat gac gaa gtt gtt aac gat				645
Asp Asp Glu Val Val Asn Asp				
210	215			

<210> 15
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Peptide

<400> 15

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
 1 5 10 15

Ser Gln Asn Gly Asn Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
 20 25 30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
 35 40 45

Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
 50 55 60

Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
65 70 75 80

Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
85 90 95

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
100 105 110

Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
115 120 125

Glu Ser Asp Lys Lys Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
130 135 140

Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
145 150 155 160

Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
165 170 175

Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
180 185 190

Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val
195 200 205

Asp Asp Glu Val Val Asn Asp
210 215

<210> 16
<211> 813
<212> DNA
<213> Artificial sequence

<220>
<223> Yeast Sup35R2E2 encoding sequence

<220>
<221> CDS
<222> (1)..(813)

<400> 16
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15 48

agc cag aac ggt aac caa caa ggt aac aac aga tac caa ggt tat
Ser Gln Asn Gly Asn Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30 96

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn 35 40 45	144
tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Tyr Gln Gln Tyr Asn 50 55 60	192
ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln 65 70 75 80	240
tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly 85 90 95	288
tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro 100 105 110	336
caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu 115 120 125	384
caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu 130 135 140	432
aac gac ttt caa aag caa cca aag cag gcc gct ccc aaa cca aag aag Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys 145 150 155 160	480
act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc Thr Leu Lys Leu Val Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr 165 170 175	528
aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu 180 185 190	576
aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu 195 200 205	624
gaa cca gtt aaa aag gag gag aaa caa gtc cag act gaa gaa aag acg Glu Pro Val Lys Lys Glu Glu Lys Gln Val Gln Thr Glu Glu Lys Thr 210 215 220	672
gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu 225 230 235 240	720
tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu 245 250 255	768
atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat Ile Lys Glu Gln Glu Glu Val Asp Asp Glu Val Val Asn Asp 260 265 270	813

<210> 17
<211> 271

<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Peptide

<400> 17

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15

Ser Gln Asn Gly Asn Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
50 55 60

Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
65 70 75 80

Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly
85 90 95

Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
100 105 110

Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu
115 120 125

Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu
130 135 140

Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys
145 150 155 160

Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr
165 170 175

Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu
180 185 190

Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu
195 200 205

Glu Pro Val Lys Lys Glu Glu Lys Gln Val Gln Thr Glu Glu Lys Thr
210 215 220

Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu
225 230 235 240

Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu
245 250 255

Ile Lys Glu Gln Glu Glu Val Asp Asp Glu Val Val Asn Asp
260 265 270

<210> 18
<211> 641
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (1) .. (633)

<400> 18
atg tct aaa aag cgg cca aag cct gga ggg tgg aac acc acc ggt gga agc 48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1 5 10 15
cgg tat ccc ggg cag gga agc cct gga ggc aac cgt tac cca cct cag 96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
20 25 30
ggc acc tgg ggg cag ccc cac ggt ggt ggc tgg gga caa ccc cat 144
Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His
35 40 45
ggg ggc agc tgg gga caa cct cat ggt ggt agt tgg ggt cag ccc cat 192
Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His
50 55 60
ggc ggt gga tgg ggc caa gga ggg ggt acc cat aat cag tgg aac aag 240
Gly Gly Trp Gly Gln Gly Gly Thr His Asn Gln Trp Asn Lys
65 70 75 80
ccc agc aaa cca aaa acc aac ctc aag cat gtg gca ggg gct gcg gca 288
Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala
85 90 95
gct ggg gca gta gtg ggg ggc ctt ggt ggc tac atg ctg ggg agc gcc 336
Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
100 105 110
gtg agc agg ccc atg atc cat ttt ggc aac gac tgg gag gac cgc tac 384
Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
115 120 125
tac cgt gaa aac atg tac cgc tac cct aac caa gtg tac tac agg cca 432
Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
130 135 140
gtg gat cag tac agc aac cag aac aac ttc gtg cac gac tgc ctg aat 480
Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Leu Asn
145 150 155 160

atc acc atc aag cag cac acg gtc acc acc acc acc aag ggg gag aac Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn 165 170 175	528
ttc acc gag acc gat gtg aag atg atg gag cgc gtg gtg gag cag atg Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met 180 185 190	576
tgc gtc acc cag tac cag aag gag tcc cag gcc tat tac gac ggg aga Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg 195 200 205	624
aga tcc agc tgataacc Arg Ser Ser 210	641
<210> 19	
<211> 211	
<212> PRT	
<213> Mouse	
<400> 19	
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser 1 5 10 15	
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln 20 25 30	
Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His 35 40 45	
Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His 50 55 60	
Gly Gly Gly Trp Gly Gln Gly Gly Thr His Asn Gln Trp Asn Lys 65 70 75 80	
Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala 85 90 95	
Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala 100 105 110	
Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr 115 120 125	
Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro 130 135 140	
Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Leu Asn 145 150 155 160	

Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn
165 170 175

Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
180 185 190

Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
195 200 205

Arg Ser Ser
210

<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus

<220>
<221> CDS
<222> (1)..(636)

<400> 20		
atg tct aag aag cgg cca aag cct gga ggg tgg aac act ggc gga agc		48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser		
1 5 10 15		
cga tac cct ggg cag ggc agc cct gga ggc aac cgt tac cca cct cag		96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln		
20 25 30		
ggt ggc ggc aca tgg ggg caa ccc cat ggt ggt ggc tgg gga cag .ccc		144
Gly Gly Thr Trp Gly Gln Pro His Gly Gly Trp Gly Gln Pro		
35 40 45		
cat ggt ggt ggc tgg gga cag ccc cat ggt ggc tgg ggt cag ccc		192
His Gly Gly Trp Gly Gln Pro His Gly Gly Trp Gly Gln Pro		
50 55 60		
cat ggt ggt ggc tgg ggt caa gga ggt ggc acc cac aat cag tgg aac		240
His Gly Gly Trp Gly Gln Gly Gly Thr His Asn Gln Trp Asn		
65 70 75 80		
aag ccc agt aag cca aaa acc aac atg aag cac atg gcc ggc gct gct		288
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala		
85 90 95		
gcg gca ggg gcc gtg gtg ggg ggc ctt ggt ggc tac atg ctg ggg agt		336
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser		
100 105 110		
gcc atg agc agg ccc atg atg cat ttt ggc aat gac tgg gag gac cgc		384
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg		
115 120 125		
tac tac cgt gaa aac atg aac cgc tac cct aac caa gtg tat tac cgg		432
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg		
130 135 140		

cca gtg gac cag tac aac aac cag aac aac ttt gtg cac gat tgt gtc	480
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val	
145 150 155 160	
aac atc acc atc aag cag cac aca gtc acc acc acc aag ggg gag	528
Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Lys Gly Glu	
165 170 175	
aac ttc acg gag acc gac atc aag ata atg gag gcg gtg gtg gag cag	576
Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Ala Val Val Glu Gln	
180 185 190	
atg tgt acc acc cag tat cag aag gag tcc cag gcc tac tac gat gga	624
Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly	
195 200 205	
aga agg tcc agc tgataacc	644
Arg Arg Ser Ser	
210	
<210> 21	
<211> 212	
<212> PRT	
<213> Mesocricetus auratus	
<400> 21	
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser	
1 5 10 15	
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln	
20 25 30	
Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	
35 40 45	
His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Trp Gly Gln Pro	
50 55 60	
His Gly Gly Gly Trp Gly Gln Gly Gly Thr His Asn Gln Trp Asn	
65 70 75 80	
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala	
85 90 95	
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser	
100 105 110	
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg	
115 120 125	
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg	
130 135 140	

Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val
145 150 155 160

Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu
165 170 175

Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Ala Val Val Glu Gln
180 185 190

Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
195 200 205

Arg Arg Ser Ser
210

<210> 22
<211> 780
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 22

Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly
1 5 10 15

Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys
20 25 30

Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Tyr Ser Tyr
35 40 45

Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr
50 55 60

Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr
65 70 75 80

Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr
85 90 95

Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys
100 105 110

Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val
115 120 125

Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly
130 135 140

Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg
145 150 155 160

Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr
165 170 175

Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg
180 185 190

Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala
195 200 205

Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp
210 215 220

Ser Arg Tyr Lys Val Asp Thr Asp Ser Lys Val Ser Val Lys Ser Ser
225 230 235 240

Ser Val Thr Cys Ala Cys Thr Ser Ser Val Asn Arg Ser Asn Ser Ser
245 250 255

Ser Ser Arg Thr Val Val Val Asn Thr Arg Val Asn Asn Arg Asn Ser
260 265 270

Gly Lys Val Val Asp Thr Ala Ser Val Arg Ala Lys Ala Asn Val Lys
275 280 285

Asp Asp Ala Asp Lys Asn Lys Ser Gly Arg Thr Gly Arg Asp Asp His
290 295 300

Lys Asp Lys Ala Asp Asp Ser Cys Val Lys Tyr Met Asn Asp Thr Val
305 310 315 320

Lys Tyr Met Ser Leu Thr Val Asp Ser Asn Val Asn Asp Trp Lys Arg
325 330 335

Asp Thr Ala Val Gly Gly Ser Asp Ser Arg Val Lys Asp His Asn Arg
340 345 350

Ala Tyr Lys Arg Ala Asp Asp Gly Val Asn Thr Asp Ser Ala Tyr Gly
355 360 365

Ser Arg Met Asn Lys Thr Asn Arg Lys Gly His Arg Tyr Gly Cys Gly
370 375 380

Arg Asn Gly Ala Gly Lys Ser Thr Met Arg Ala Ala Asn Gly Asp Gly
385 390 395 400

Asp Lys Asp Thr Arg Thr Cys Val His Lys Gly Gly Asp Asp Val Ser
405 410 415

Ala Asp Ser Thr Ser Arg Ala Ala Ser Val Gly Asp Arg Arg Ala
420 425 430

Thr Val Gly Ser Ser Gly Gly Trp Lys Met Lys Ala Arg Ala Met Lys
435 440 445

Ala Asp Asp Thr Asn His Asp Val Ser Asn Val Lys Trp Tyr His Thr
450 455 460

Asp Thr Ser Val Ser His Asp Ser Gly Asp Thr Val Cys Thr Asp His
465 470 475 480

Tyr Asn Lys Lys Ala Tyr Tyr Lys Gly Asn Ala Ala Val Lys Ala Lys
485 490 495

Ser Tyr Tyr Thr Thr Asp Ser Asn Ala Met Arg Gly Thr Gly Val Lys
500 505 510

Ser Asn Thr Arg Ala Val Ala Lys Met Thr Asp Val Thr Ser Tyr Gly
515 520 525

Ala Lys Ser Ser His Val Ser Cys Ser Ser Ser Arg Val Ala Cys
530 535 540

Gly Asn Gly Ala Gly Lys Ser Thr Leu Thr Gly Val Asn Gly Lys Val
545 550 555 560

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr
565 570 575

Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser
580 585 590

Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala
595 600 605

Val Gly Arg Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys
610 615 620

Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp
625 630 635 640

His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly
645 650 655

Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala
660 665 670

Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser
675 680 685

Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His
690 695 700

Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser
705 710 715 720

Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala
725 730 735

Ser Asn Ala Lys Ser Val Asp Asp Asp Ser Ala Asn Lys Val Lys
740 745 750

Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Arg Tyr Trp
755 760 765

Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp
770 775 780

<210> 23

<211> 1075

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 23

Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu
1 5 10 15

Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg
20 25 30

Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp
35 40 45

Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr
50 55 60

Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Lys Thr Asn Lys Lys Pro
65 70 75 80

Ser Ile Ser Ala Lys Leu His His Ser Lys Lys Ser Thr Pro Val Val
85 90 95

Val Val Pro Pro Thr Ser Ser Thr Pro Asp Ser Lys Asn Ser Thr Thr
100 105 110

Tyr Ala Pro Arg Val Ser Ser Asp Ser Phe Thr Val Ala Thr Pro Leu
115 120 125

Ser Leu Gln Ser Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val
130 135 140

Ser Ser Gln Ile Thr Ala Ser Ser Ser Lys Thr Thr Asp Val Gly Asn
145 150 155 160

Ala Thr Ser Ala Asn Ile Trp Ser Ala Asn Ala Glu Ser Asn Thr Ser
165 170 175

Ser Ser Pro Leu Phe Asp Tyr Pro Leu Ala Thr Ser Tyr Phe Glu Pro
180 185 190

Leu Thr Arg Phe Lys Ser Thr Asp Asn Tyr Thr Leu Pro Gln Thr Ala
195 200 205

Gln Leu Asn Ser Phe Leu Glu Lys Asn Gly Asn Pro Asn Ile Trp Ser
210 215 220

Ser Ala Gly Asn Ser Asn Thr Asp His Leu Asn Thr Pro Ile Val Asn
225 230 235 240

Arg Gln Arg Ser Gln Ser Gln Asn Thr Thr Asn Arg Val Tyr Thr Asp
245 250 255

Ala Pro Tyr Tyr Gln Gln Pro Ala Gln Asn Tyr Gln Val Tyr Val Pro
260 265 270

Pro Arg Val Pro Lys Ser Thr Ser Ile Ser Pro Val Ile Leu Asp Asp
275 280 285

Val Asp Pro Ala Ser Ile Asn Trp Ile Thr Ala Asn Gln Lys Val Pro
290 295 300

Leu Val Asn Gln Ile Ser Ala Leu Leu Pro Thr Asn Thr Ile Ser Ile
305 310 315 320

Ser Asn Val Phe Pro Leu Gln Pro Thr Gln Gln His Gln Gln Asn Ala
325 330 335

Val Asn Leu Thr Ser Thr Ser Leu Ala Thr Leu Cys Ser Gln Tyr Gly
340 345 350

Lys Val Leu Ser Ala Arg Thr Leu Arg Gly Leu Asn Met Ala Leu Val
355 360 365

Glu Phe Ser Thr Val Glu Ser Ala Ile Cys Ala Leu Glu Ala Leu Gln
370 375 380

Gly Lys Glu Leu Ser Lys Val Gly Ala Pro Ser Thr Val Ser Phe Ala
385 390 395 400

Arg Val Leu Pro Met Tyr Glu Gln Pro Leu Asn Val Asn Gly Phe Asn
405 410 415

Asn Thr Pro Lys Gln Pro Leu Leu Gln Glu Gln Leu Asn His Gly Val
420 425 430

Leu Asn Tyr Gln Lys Gln Gln Ser Leu Gln Gln Pro Glu Leu Gln Gln
435 440 445

Gln Pro Thr Ser Phe Asn Gln Pro Asn Leu Thr Tyr Cys Asn Pro Thr
450 455 460

Gln Asn Leu Ser His Leu Gln Leu Ser Ser Asn Glu Asn Glu Pro Tyr
465 470 475 480

Pro Phe Pro Leu Pro Pro Ser Leu Ser Asp Ser Lys Lys Asp Ile
485 490 495

Leu His Thr Ile Ser Ser Phe Lys Leu Glu Tyr Asp His Leu Glu Leu
500 505 510

Asn His Leu Leu Gln Asn Ala Leu Lys Asn Lys Gly Val Ser Asp Thr
515 520 525

Asn Tyr Phe Gly Pro Leu Pro Glu His Asn Ser Lys Val Pro Lys Arg
530 535 540

Lys Asp Thr Phe Asp Ala Pro Lys Leu Arg Glu Leu Arg Lys Gln Phe
545 550 555 560

Asp Ser Asp Ser Leu Ser Thr Ile Glu Met Glu Gln Leu Ala Ile Val
565 570 575

Met Leu Asp Gln Leu Pro Glu Leu Ser Ser Asp Tyr Leu Gly Asn Thr
580 585 590

Val Ile Gln Lys Leu Phe Glu Asn Ser Ser Asn Ile Ile Arg Asp Ile
595 600 605

Met Leu Arg Lys Cys Asn Lys Tyr Leu Thr Ser Met Gly Val His Lys
610 615 620

Asn Gly Thr Trp Val Cys Gln Lys Ile Ile Lys Met Ala Asn Thr Pro
625 630 635 640

Arg Gln Ile Asn Leu Val Thr Ser Gly Val Ser Asp Tyr Cys Thr Pro
645 650 655

Leu Phe Asn Asp Gln Phe Gly Asn Tyr Val Ile Gln Gly Ile Leu Lys
660 665 670

Phe Gly Phe Pro Trp Asn Ser Phe Ile Phe Glu Ser Val Leu Ser His
675 680 685

Phe Trp Thr Ile Val Gln Asn Arg Tyr Gly Ser Arg Ala Val Arg Ala
690 695 700

Cys Leu Glu Ala Asp Ser Ile Ile Thr Gln Cys Gln Leu Leu Thr Ile
705 710 715 720

Thr Ser Leu Ile Ile Val Leu Ser Pro Tyr Leu Ala Thr Asp Thr Asn
725 730 735

Gly Thr Leu Leu Ile Thr Trp Leu Leu Asp Thr Cys Thr Leu Pro Asn
740 745 750

Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys
755 760 765

Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn
770 775 780

Leu Arg Gly Gly Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His
785 790 795 800

Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile
805 810 815

Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr
820 825 830

Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile
835 840 845

Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu
850 855 860

Leu Glu Glu Val Gly Lys Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser
865 870 875 880

Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly
885 890 895

Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg
900 905 910

His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu
915 920 925

Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn
930 935 940

Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn
945 950 955 960

Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile
965 970 975

Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val
980 985 990

Ser Asn Asn Asn Asn Tyr Asn Asn Ser Gly Tyr Ser Ser Gln Met
995 1000 1005

Asn Pro Leu Ser Arg Ser Val Ser His Asn Asn Asn Asn Asn Asn Thr
1010 1015 1020

Asn Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn Asn Asn Asn
1025 1030 1035

Asn
1040 1045 1050

Ser Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asp Thr Ser Leu Tyr
1055 1060 1065

Arg Tyr Arg Ser Tyr Gly Tyr
1070 1075

<210> 24
<211> 76
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 24

Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Lys Ser Tyr Ser
1 5 10 15

Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
20 25 30 35

Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
35 40 45

Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
50 55 60

Ala Ala Cys Ala Ala Cys Cys Cys Thr Met Asp Met
65 70 75

<210> 25
<211> 380
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 25

Met Ser Ser Asp Asp Asn Asp Tyr Gly Asp Asp Lys Thr Thr Thr Val
1 5 10 15

Lys Lys Asn Lys Ala Gly Ser Gly Thr Ser Asp Ala Ala Ala Ser Ser
20 25 30

Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
35 40 45

Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
50 55 60

Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
65 70 75 80

Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Val Thr
85 90 95

Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Asn Gly Gly Asn
100 105 110

Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
115 120 125

Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
130 135 140

Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
145 150 155 160

Asp Asp Lys Thr Gly Lys Val Gly Gly Asp Val Arg Lys Ser Trp
165 170 175

Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Val Thr
180 185 190

Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Asn Lys Asp Lys Asp
195 200 205

Arg Lys Lys Arg Ala Arg His Met Lys Ser Ser Asn Asn Gly Gly Asn
210 215 220

Asn Gly Gly Asn Asn Met Asn Arg Arg Gly Gly Asn Gly Asn Gly Asp
225 230 235 240

Asn Met Tyr Asn Met Met Gly Gly Tyr Asn Met Met Asn Ala Met Thr
245 250 255

Asp Tyr Tyr Lys Met Tyr Tyr Met Lys Thr Gly Met Asp Tyr Thr Met
260 265 270

Tyr Met Met Ala Met Met Met Gly Ala Met Asn Ala Met Thr Asn Asp
275 280 285

Ser Asn Ala Thr Gly Ser Ala Ser Asp Ser Asp Asn Asn Lys Ser Asn
290 295 300

Asp Val Thr Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Asn Asn Gly
305 310 315 320

Lys Gly Ser Tyr Asn Asp Asp His Asn Ser Gly Tyr Gly Tyr Asn Arg
325 330 335

Asp Arg Gly Asp Arg Asp Arg Asn Asp Arg Asp Arg Asp Tyr Asn His
340 345 350

Arg Ser Gly Gly Asn His Arg Arg Asn Gly Arg Gly Gly Arg Gly Gly
355 360 365

Tyr Asn Arg Arg Asn Asn Gly Tyr His Tyr Asn Arg
370 375 380

<210> 26
<211> 256
<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

Met Ser Ala Thr His Val Ser Val Val Asp Ala Val His Ala Asp Ala
1 5 10 15

Val Ser Ala Ser Ala Ala Asn Asp Val Ser Asn Ala Tyr Gly Ser His
20 25 30

Ser Val Asp Tyr Ala His His Tyr Tyr Gly His Met His Gly Arg
35 40 45

Met His His Arg Gly Ser Asn Thr Arg Val Arg Asp Val Ser Asn Gly
50 55 60

Gly Met Lys Val Lys Asn Gly Ala Val Ala Ser Ala Ala Lys Ala Val
65 70 75 80

His Gly Lys Ser Ala Asn Val Val Tyr Ser Lys Ala Lys Arg Tyr Arg
85 90 95

Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr
100 105 110

Thr Ser Ser Val Asn Thr Arg Asp Asp Gly Thr Gly Ala Ser Val Ala
115 120 125

Arg Asn Asn Arg Gly Ser Val Thr Val Arg Asp Asp Asn Arg Arg Ser
130 135 140

Asn Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg
145 150 155 160

Gly Gly Ser Arg Gly Gly Gly Arg Gly Gly Gly Arg Gly Gly
165 170 175

Tyr Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Tyr Ser Arg Gly Gly
180 185 190

Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Ser Asp Gly Gly Tyr Asp Ser
195 200 205

Arg Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Arg Asn Asp Tyr Gly
210 215 220

Arg Gly Ser Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Gly Arg Gly Asp
225 230 235 240

Tyr Gly Arg Asp Ala Tyr Arg Thr Arg Asp Ala Arg Arg Ser Thr Arg
245 250 255

<210> 27
<211> 286
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 27

Met Ser Asp Ile Glu Glu Gly Thr Pro Thr Asn Asn Gly Gln Gln Lys
1 5 10 15

Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg
20 25 30

His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe
35 40 45

Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Val Val Ser
50 55 60

Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile
65 70 75 80

Val Thr Gln Gln Glu Gly Arg Asn Lys Ile Gln Ala Cys Leu Asn Ala
85 90 95

Pro Asp Asp Glu Glu Asp Glu Glu Asp Gly Asp Asp Asp Asp
100 105 110

Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln
115 120 125

Gln Gln Pro Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser
130 135 140

Leu Gly His Leu Asn Gln Asp Gln Val Pro Ala Gly Ala Leu Lys Gln
145 150 155 160

Glu Val Lys Ser Gln Leu Leu Gly Gly Ala Asn Pro Asn Gln Asn Ser
165 170 175

Met Ile Gln Gln Gln His His Thr Gln Asn Ser Gln Pro Gln Gln
180 185 190

Gln Gln Gln Gln Pro Gln Gln Met Ser Gln Gln Gln Met Ser
195 200 205

Gln His Pro Arg Pro Gln Gln Gly Ile Pro His Pro Gln Gln Ser Gln
210 215 220

Pro Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln
225 230 235 240

Gln Gln Gln Gln Pro Leu Thr Gly Ile His Gln Pro His Gln Gln
245 250 255

Ala Phe Ala Asn Ala Ala Ser Pro Tyr Leu Asn Ala Glu Gln Asn Ala
260 265 270

Ala Tyr Gln Gln Tyr Phe Gln Glu Pro Gln Gln Gly Gln Tyr
275 280 285

<210> 28
<211> 414
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 28

Met Ala Lys Thr Thr Lys Val Lys Gly Asn Lys Lys Glu Val Lys Ala
1 5 10 15

Ser Lys Gln Ala Lys Glu Glu Lys Ala Lys Ala Val Ser Ser Ser Ser
20 25 30

Ser Glu Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Glu
35 40 45

Ser Glu Ser Glu Ser Glu Ser Ser Ser Ser Ser Ser Ser Asp Ser
50 55 60

Glu Ser Ser Ser Ser Ser Ser Asp Ser Glu Ser Glu Ala Glu Thr
65 70 75 80

Lys Lys Glu Glu Ser Lys Asp Ser Ser Ser Ser Ser Ser Asp Ser Ser
85 90 95

Ser Asp Glu Glu Glu Glu Glu Lys Glu Glu Thr Lys Lys Glu Glu
100 105 110

Ser Lys Glu Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Asp
115 120 125

Ser Glu Ser Glu Lys Glu Glu Ser Asn Asp Lys Lys Arg Lys Ser Glu
130 135 140

Asp Ala Glu Glu Glu Glu Asp Glu Glu Ser Ser Asn Lys Lys Gln Lys
145 150 155 160

Asn Glu Glu Thr Glu Glu Pro Ala Thr Ile Phe Val Gly Arg Leu Ser
165 170 175

Trp Ser Ile Asp Asp Glu Trp Leu Lys Lys Glu Phe Glu His Ile Gly
180 185 190

Gly Val Ile Gly Ala Arg Val Ile Tyr Glu Arg Gly Thr Asp Arg Ser
195 200 205

Arg Gly Tyr Gly Tyr Val Asp Phe Glu Asn Lys Ser Tyr Ala Glu Lys
210 215 220

Ala Ile Gln Glu Met Gln Gly Lys Glu Ile Asp Gly Arg Pro Ile Asn
225 230 235 240

Cys Asp Met Ser Thr Ser Lys Pro Ala Gly Asn Asn Asp Arg Ala Lys
245 250 255

Lys Phe Gly Asp Thr Pro Ser Glu Pro Ser Asp Thr Leu Phe Leu Gly
260 265 270

Asn Leu Ser Phe Asn Ala Asp Arg Asp Ala Ile Phe Glu Leu Phe Ala
275 280 285

Lys His Gly Glu Val Val Ser Val Arg Ile Pro Thr His Pro Glu Thr
290 295 300

Glu Gln Pro Lys Gly Phe Gly Tyr Val Gln Phe Ser Asn Met Glu Asp
305 310 315 320

Ala Lys Lys Ala Leu Asp Ala Leu Gln Gly Glu Tyr Ile Asp Asn Arg
325 330 335

Pro Val Arg Leu Asp Phe Ser Ser Pro Arg Pro Asn Asn Asp Gly Gly
340 345 350

Arg Gly Gly Ser Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Gly
355 360 365

Asn Arg Gly Phe Gly Gly Arg Gly Ala Arg Gly Gly Arg Gly Gly
370 375 380

Phe Arg Pro Ser Gly Ser Gly Ala Asn Thr Ala Pro Leu Gly Arg Ser
385 390 395 400

Arg Asn Thr Ala Ser Phe Ala Gly Ser Lys Lys Thr Phe Asp
405 410

<210> 29
<211> 405
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 29

Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
1 5 10 15

Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
20 25 30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
35 40 45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
50 55 60

Gln Asp Arg Ala Ala Gly Gly Ser Ser Phe Met Asn Thr Leu Met
65 70 75 80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
85 90 95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
100 105 110

Gly Phe Asp Val Gly Thr Cys Met Ser Met Leu Ser Gly Ser Gly Gly
115 120 125

Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
130 135 140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly
145 150 155 160

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
165 170 175

Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
180 185 190

Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
195 200 205

Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
210 215 220

Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225 230 235 240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
245 250 255

Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
260 265 270

Met Ala Gln Ser Tyr Leu Gly Gly Gln Thr Gln Ser Asn Gln Gln
275 280 285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
290 295 300

Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gln Gly
305 310 315 320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
325 330 335

Gly Asn Asn Ser Asn Ser Asn Ser Tyr Gly Gly Gln Gln Gln Ala
340 345 350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
355 360 365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
370 375 380

Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
385 390 395 400

Asn Gln Asn Arg Tyr

<210> 30
<211> 964
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 30

Met Pro Glu Gln Ala Gln Gln Gly Glu Gln Ser Val Lys Arg Arg Arg
1 5 10 15

Val	Thr	Arg	Ala	Cys	Asp	Glu	Cys	Arg	Lys	Lys	Lys	Val	Lys	Cys	Asp
20							25					30			
Gly Gln Gln Pro Cys Ile His Cys Thr Val Tyr Ser Tyr Glu Cys Thr															
35						40					45				
Tyr Lys Lys Pro Thr Lys Arg Thr Gln Asn Ser Gly Asn Ser Gly Val															
50					55				60						
Leu Thr Leu Gly Asn Val Thr Thr Gly Pro Ser Ser Ser Thr Val Val															
65					70			75			80				
Ala Ala Ala Ala Ser Asn Pro Asn Lys Leu Leu Ser Asn Ile Lys Thr															
85						90				95					
Glu Arg Ala Ile Leu Pro Gly Ala Ser Thr Ile Pro Ala Ser Asn Asn															
100						105				110					
Pro Ser Lys Pro Arg Lys Tyr Lys Thr Lys Ser Thr Arg Leu Gln Ser															
115						120				125					
Lys Ile Asp Arg Tyr Lys Gln Ile Phe Asp Glu Val Phe Pro Gln Leu															
130					135				140						
Pro Asp Ile Asp Asn Leu Asp Ile Pro Val Phe Leu Gln Ile Phe His															
145					150			155			160				
Asn Phe Lys Arg Asp Ser Gln Ser Phe Leu Asp Asp Thr Val Lys Glu															
165						170				175					
Tyr Thr Leu Ile Val Asn Asp Ser Ser Ser Pro Ile Gln Pro Val Leu															
180						185				190					
Ser Ser Asn Ser Lys Asn Ser Thr Pro Asp Glu Phe Leu Pro Asn Met															
195					200				205						
Lys Ser Asp Ser Asn Ser Ala Ser Ser Asn Arg Glu Gln Asp Ser Val															
210					215				220						
Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu															
225					230			235			240				
Pro Pro Lys Ala Ile Ala Leu Gln Phe Val Lys Ser Thr Trp Glu His															
245						250				255					
Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln															
260						265				270					

Leu Asp Glu Leu Tyr Glu Thr Asp Pro Asn Asn Tyr Thr Ser Lys Gln
275 280 285

Met Gln Phe Leu Pro Leu Cys Tyr Ala Ala Ile Ala Val Gly Ala Leu
290 295 300

Phe Ser Lys Ser Ile Val Ser Asn Asp Ser Ser Arg Glu Lys Phe Leu
305 310 315 320

Gln Asp Glu Gly Tyr Lys Tyr Phe Ile Ala Ala Arg Lys Leu Ile Asp
325 330 335

Ile Thr Asn Ala Arg Asp Leu Asn Ser Ile Gln Ala Ile Leu Met Leu
340 345 350

Ile Ile Phe Leu Gln Cys Ser Ala Arg Leu Ser Thr Cys Tyr Thr Tyr
355 360 365

Ile Gly Val Ala Met Arg Ser Ala Leu Arg Ala Gly Phe His Arg Lys
370 375 380

Leu Ser Pro Asn Ser Gly Phe Ser Pro Ile Glu Ile Glu Met Arg Lys
385 390 395 400

Arg Leu Phe Tyr Thr Ile Tyr Lys Leu Asp Val Tyr Ile Asn Ala Met
405 410 415

Leu Gly Leu Pro Arg Ser Ile Ser Pro Asp Asp Phe Asp Gln Thr Leu
420 425 430

Pro Leu Asp Leu Ser Asp Glu Asn Ile Thr Glu Val Ala Tyr Leu Pro
435 440 445

Glu Asn Gln His Ser Val Leu Ser Ser Thr Gly Ile Ser Asn Glu His
450 455 460

Thr Lys Leu Phe Leu Ile Leu Asn Glu Ile Ile Ser Glu Leu Tyr Pro
465 470 475 480

Ile Lys Lys Thr Ser Asn Ile Ile Ser His Glu Thr Val Thr Ser Leu
485 490 495

Glu Leu Lys Leu Arg Asn Trp Leu Asp Ser Leu Pro Lys Glu Leu Ile
500 505 510

Pro Asn Ala Glu Asn Ile Asp Pro Glu Tyr Glu Arg Ala Asn Arg Leu
515 520 525

Leu His Leu Ser Phe Leu His Val Gln Ile Ile Leu Tyr Arg Pro Phe
530 535 540

Ile His Tyr Leu Ser Arg Asn Met Asn Ala Glu Asn Val Asp Pro Leu
545 550 555 560

Cys Tyr Arg Arg Ala Arg Asn Ser Ile Ala Val Ala Arg Thr Val Ile
565 570 575

Lys Leu Ala Lys Glu Met Val Ser Asn Asn Leu Leu Thr Gly Ser Tyr
580 585 590

Trp Tyr Ala Cys Tyr Thr Ile Phe Tyr Ser Val Ala Gly Leu Leu Phe
595 600 605

Tyr Ile His Glu Ala Gln Leu Pro Asp Lys Asp Ser Ala Arg Glu Tyr
610 615 620

Tyr Asp Ile Leu Lys Asp Ala Glu Thr Gly Arg Ser Val Leu Ile Gln
625 630 635 640

Leu Lys Asp Ser Ser Met Ala Ala Ser Arg Thr Tyr Asn Leu Leu Asn
645 650 655

Gln Ile Phe Glu Lys Leu Asn Ser Lys Thr Ile Gln Leu Thr Ala Leu
660 665 670

His Ser Ser Pro Ser Asn Glu Ser Ala Phe Leu Val Thr Asn Asn Ser
675 680 685

Ser Ala Leu Lys Pro His Leu Gly Asp Ser Leu Gln Pro Pro Val Phe
690 695 700

Phe Ser Ser Gln Asp Thr Lys Asn Ser Phe Ser Leu Ala Lys Ser Glu
705 710 715 720

Glu Ser Thr Asn Asp Tyr Ala Met Ala Asn Tyr Leu Asn Asn Thr Pro
725 730 735

Ile Ser Glu Asn Pro Leu Asn Glu Ala Gln Gln Asp Gln Val Ser
740 745 750

Gln Gly Thr Thr Asn Met Ser Asn Glu Arg Asp Pro Asn Asn Phe Leu
755 760 765

Ser Ile Asp Ile Arg Leu Asp Asn Asn Gly Gln Ser Asn Ile Leu Asp
770 775 780

Ala Thr Asp Asp Val Phe Ile Arg Asn Asp Gly Asp Ile Pro Thr Asn
785 790 795 800

Ser Ala Phe Asp Phe Ser Ser Ser Lys Ser Asn Ala Ser Asn Asn Ser
805 810 815

Asn Pro Asp Thr Ile Asn Asn Asn Tyr Asn Asn Val Ser Gly Lys Asn
820 825 830

Asn Asn Asn Asn Ile Thr Asn Asn Ser Asn Asn His Asn Asn
835 840 845

Asn Asn Asn Asp Asn
850 855 860

Asn Asn Asn Asn Asn Ser Gly Asn Ser Ser Asn Asn Asn Asn Asn Asn
865 870 875 880

Asn Asn Asn Lys Asn Asn Asp Phe Gly Ile Lys Ile Asp Asn Asn
885 890 895

Ser Pro Ser Tyr Glu Gly Phe Pro Gln Leu Gln Ile Pro Leu Ser Gln
900 905 910

Asp Asn Leu Asn Ile Glu Asp Lys Glu Glu Met Ser Pro Asn Ile Glu
915 920 925

Ile Lys Asn Glu Gln Asn Met Thr Asp Ser Asn Asp Ile Leu Gly Val.
930 935 940

Phe Asp Gln Leu Asp Ala Gln Leu Phe Gly Lys Tyr Leu Pro Leu Asn
945 950 955 960

Tyr Pro Ser Glu

<210> 31
<211> 758
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 31

Met Asp Asn Thr Thr Asn Ile Asn Thr Asn Glu Arg Ser Ser Asn Thr
1 5 10 15

Asp Phe Ser Ser Ala Pro Asn Ile Lys Gly Leu Asn Ser His Thr Gln
20 25 30

Leu Asn Phe Asp Ala Asp Ser Arg Val Phe Val Ser Asp Val Met Ala
35 40 45

Lys Asn Ser Lys Gln Leu Leu Tyr Ala His Ile Tyr Asn Tyr Leu Ile
50 55 60

Lys Asn Asn Tyr Trp Asn Ser Ala Ala Lys Phe Leu Ser Glu Ala Asp
65 70 75 80

Leu Pro Leu Ser Arg Ile Asn Gly Ser Ala Ser Gly Gly Lys Thr Ser
85 90 95

Lys Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly
100 105 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp
115 120 125

Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu
130 135 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu
145 150 155 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met
165 170 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln
180 185 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly
195 200 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg
210 215 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn
225 230 235 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Asn Asn Tyr
245 250 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala
260 265 270

Gln Pro Gln Gln Ser Ser Gln Gln Ile Gln Gln Pro Gln His Gln
275 280 285

Pro Gln His Gln Pro Gln
290 295 300

Gln
305 310 315 320

Gln Gln Gln His Gln Gln Gln Gln Thr Pro Tyr Pro Ile Val Asn
325 330 335

Pro Gln Met Val Pro His Ile Pro Ser Glu Asn Ser His Ser Thr Gly
340 345 350

Leu Met Pro Ser Val Pro Pro Thr Asn Gln Gln Phe Asn Ala Gln Thr
355 360 365

Gln Ser Ser Met Phe Ser Asp Gln Gln Arg Phe Phe Gln Tyr Gln Leu
370 375 380

His His Gln Asn Gln Gly Gln Ala Pro Ser Phe Gln Gln Ser Gln Ser
385 390 395 400

Gly Arg Phe Asp Asp Met Asn Ala Met Lys Met Phe Phe Gln Gln Gln
405 410 415

Ala Leu Gln Gln Asn Ser Leu Gln Gln Asn Leu Gly Asn Gln Asn Tyr
420 425 430

Gln Ser Asn Thr Arg Asn Asn Thr Ala Glu Glu Thr Thr Pro Thr Asn
435 440 445

Asp Asn Asn Ala Asn Gly Asn Ser Leu Leu Gln Glu His Ile Arg Ala
450 455 460

Arg Phe Asn Lys Met Lys Thr Ile Pro Gln Gln Met Lys Asn Gln Ser
465 470 475 480

Thr Val Ala Asn Pro Val Val Ser Asp Ile Thr Ser Gln Gln Gln Tyr
485 490 495

Met His Met Met Met Gln Arg Met Ala Ala Asn Gln Gln Leu Gln Asn
500 505 510

Ser Ala Phe Pro Pro Asp Thr Asn Arg Ile Ala Pro Ala Asn Asn Thr
515 520 525

Met Pro Leu Gln Pro Gly Asn Met Gly Ser Pro Val Ile Glu Asn Pro
530 535 540

Gly Met Arg Gln Thr Asn Pro Ser Gly Gln Asn Pro Met Ile Asn Met
545 550 555 560

Gln Pro Leu Tyr Gln Asn Val Ser Ser Ala Met His Ala Phe Ala Pro
565 570 575

Gln Gln Gln Phe His Leu Pro Gln His Tyr Lys Thr Asn Thr Ser Val
580 585 590

Pro Gln Asn Asp Ser Thr Ser Val Phe Pro Leu Pro Asn Asn Asn Asn
595 600 605

Asn Ser Asn Asn
610 615 620

Ser Asn Ser Asn Asn
625 630 635 640

Thr Pro Thr Val Ser Gln Pro Ser Ser Lys Cys Thr Ser Ser Ser Ser
645 650 655

Thr Thr Pro Asn Ile Thr Thr Ile Gln Pro Lys Arg Lys Gln Arg
660 665 670

Val Gly Lys Thr Lys Thr Lys Glu Ser Arg Lys Val Ala Ala Ala Gln
675 680 685

Lys Val Met Lys Ser Lys Lys Leu Glu Gln Asn Gly Asp Ser Ala Ala
690 695 700

Thr Asn Phe Ile Asn Val Thr Pro Lys Asp Ser Gly Gly Lys Gly Thr
705 710 715 720

Val Lys Val Gln Asn Ser Asn Ser Gln Gln Gln Lys Asn Gly Ser Phe
725 730 735

Ser Met Asp Thr Glu Thr Phe Asp Ile Phe Asn Ile Gly Asp Phe Ser
740 745 750

Pro Asp Leu Met Asp Ser
755

<210> 32
<211> 750
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 32

Met Thr Ser Val Asn Arg Ser Asn Asn Thr Arg Ser Met Ser Ala Ser
1 5 10 15

Arg Ser Ala Thr Ser Arg Val Arg Asn Thr Thr Ala Asn Ser Ser Asp
20 25 30

Val Asn Ser Ser Lys Arg Asn Ser Asn Ser Val Tyr Asp Asp Asn Ser
35 40 45

Ser Lys Arg Arg Ser Arg Arg Ser Asp Gly Lys Asn Asn Asp His Thr
50 55 60

Tyr Arg Thr Thr Val Lys Ser Lys Asn Ser Arg Tyr Val Ser Ser Ser
65 70 75 80

Lys Arg Ala Lys Arg Asn Ser Val Gly Thr Ser Ser Ala Ser Lys Ser
85 90 95

Ser Asn Gly Gly Ser Ala His Lys Trp Ser Asn Met Lys Asn Val Ser
100 105 110

Asn Ser Ala Val Asp Ala Gly Ser Asp Ser Lys Ser Val Gly Gly Arg
115 120 125

Lys Ser Asn Asn Ser Asn Asp Lys Asp Asn Ser Ala Arg Asp Asp Asn
130 135 140

Asn Ser Gly Asn Asn Asn Asn Asn His Ser Ser Asn Asn Asn
145 150 155 160

Asp Asn Asn Asn Asn Asn Asp Asp Asn Asn Asn Asn Asn Asn Ser
165 170 175

Asn Ser Arg Asp Asn Asn Asn Ser Asp Asp Ser Asn Arg Asn Asp
180 185 190

Ser Cys Lys Ala Ser Asn Lys Arg Ser Gly Ala Lys Tyr Lys Val Val
195 200 205

Lys Arg Cys Ser Thr Asn Ser Thr Thr Lys Ser Trp Thr Tyr Lys Asn
210 215 220

Thr Asp Val Asn Asn Tyr Val Thr Thr Ala Ser His Asp Val Gly
225 230 235 240

Val Tyr Arg Arg Arg Trp Val Tyr Gly Thr Thr Asp Val Lys Asn Ser
245 250 255

Asn Met Asp Val Cys Cys Thr His Val Val Ser Ser Thr Met Ser Asp
260 265 270

Ser Lys Tyr Ser Thr Trp Arg Gly Asp Ser Arg Met Ala Ala Tyr Ser
275 280 285

Ser Asp Tyr Lys Ser Ala His Trp Tyr Thr Ala Met Lys Tyr Tyr Asn
290 295 300

His Gly Lys Tyr Tyr His Met Ser Thr Val Asn Thr Ala Val Asn Gly
305 310 315 320

Lys Ser Val Cys Thr Thr Ser Tyr Met Val Asp Asn Tyr Arg Ala Val
325 330 335

Arg Asn Asn Gly Asn Arg Asn Ser Tyr Lys His Ser Ala Met Ser Ser
340 345 350

Asp Asn Val Val Ser Tyr Lys Gly Asp Ala Asn Gly Cys Asn Asn Ala
355 360 365

Asp Met Val Asn Asp Lys Tyr Arg His Gly Ser Ala Ser His Val Gly
370 375 380

Gly Lys Asn Ala Lys Tyr Lys Arg Lys Asp Lys Lys Arg Lys Lys Ser
385 390 395 400

Ser Asn Asn Asp Ser Ser Val Thr Ser Ser Thr Gly Asn Ser Arg Asn
405 410 415

Asp Asn Asp Asp Asp Met Ser Ser Thr Thr Ser Ser Asp His Asp Ala
420 425 430

Asn Asp Asp Thr Arg Arg Ser Met Thr Asn Ala Trp Thr Lys Asn Met
435 440 445

Thr Ser Lys Cys Gly Val Arg Lys His Gly Gly Ala His Trp Tyr Ser
450 455 460

Cys Lys Ser Ser Ser Asp Val Ser Lys Trp Met Val Lys Arg Ala Trp
465 470 475 480

Asp Thr Met Val Thr Met Asn Val Val Tyr Asp Asn Thr Ser Asn Ser
485 490 495

Gly Asp Cys Asp Asp Tyr Asp Lys Ser Ser Asn Gly Gly Cys Trp Gly
500 505 510

Thr Trp Asp Thr Cys Lys Asn Thr His Ser Ser Ser Asp Asn Gly Lys
515 520 525

Asp Tyr Met Ala Asp Ser Thr Asp Gly Asp Lys Asp Asn Gly Lys Trp
530 535 540

Lys Arg Ala Cys Arg Thr Arg Ser Arg Ser Gly Val Arg Asn Asp Tyr
545 550 555 560

Arg Ser Ser Asn Thr Asn Gly Ser Val Lys Cys Asn His Asn Asn Val
565 570 575

Gly Ala Ser Asp Ser Ala Arg Ser Asn Asn Thr Asp His Ala Val Ser
580 585 590

Val Asn Gly Asp Asn His Tyr Val Gly Tyr Lys Lys Arg Ala Asp Tyr
595 600 605

Thr Cys Asp Lys Asn Gly Ser Ala Ser Tyr Thr Thr Trp Tyr Val Asn
610 615 620

Ser Asn Asn Thr Asn Asp Asn Asn Tyr Asn Ser Lys Asn Gly Cys Lys
625 630 635 640

Ser Asp Tyr Asp Lys Thr Thr Tyr Val Asp Ala Thr Ser Trp Arg His
645 650 655

Ser Ala Arg Lys Ala Asn Arg Arg Ala Cys Thr Thr Arg Arg Lys Ser
660 665 670

Lys Asp Asn Val Met Ala Ala Thr Arg Gly Thr Arg Tyr Tyr Asn Lys
675 680 685

Val Arg Thr Gly Asn Val Ala Thr His Asn Thr Trp Arg Thr His Val
690 695 700

Asp Val Ser Val Met Lys Ala Lys Ser Ala Ser Arg Ser Arg Arg Asn
705 710 715 720

Tyr Val Val Ser Asp Asp Asp Ala Met Lys Lys Lys Ala Lys Lys Thr
725 730 735

Ser Thr Arg Val Ser Cys Thr Lys Gly Arg His Cys Thr Asp
740 745 750

<210> 33
<211> 710
<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 33

Met Asp Asn Lys Arg Tyr Asn Gly Asn Ser Asn Val Asp Gly Thr Tyr
1 5 10 15

Asp Arg Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val
20 25 30

Ser Asp Lys Arg Gly Arg Ser Ser Ser Thr Ser Lys Gly Ser Tyr Arg
35 40 45

Thr Arg Ala Gly Arg Ser Asp Thr Thr Asn Ser Ser Ala Lys His His
50 55 60

Ser Lys Lys Ser Thr Val Val Val Val Thr Ser Ser Thr Asp Ser Asn
65 70 75 80

Ser Thr Thr Tyr Ala Arg Val Ser Ser Asp Ser Thr Val Ala Thr Ser
85 90 95

Ser Thr Thr Thr Arg Thr Arg Asn Asn Thr Val Ser Ser Thr
100 105 110

Ala Ser Ser Ser Thr Thr Asp Val Gly Asn Ala Thr Ser Ala Asn Trp
115 120 125

Ser Ala Asn Ala Ser Asn Thr Ser Ser Ser Asp Tyr Ala Thr Ser Tyr
130 135 140

Thr Arg Lys Ser Thr Asp Asn Tyr Thr Thr Ala Asn Ser Lys Asn Gly
145 150 155 160

Asn Asn Trp Ser Ser Ala Gly Asn Ser Asn Thr Asp His Asn Thr Val
165 170 175

Asn Arg Arg Ser Ser Ser Thr Thr Asn Arg Val Tyr Thr Asp Ala Tyr
180 185 190

Tyr Ala Asn Tyr Val Val Arg Val Lys Ser Thr Ser Ser Val Asp Asp
195 200 205

Val Asp Ala Ser Asn Trp Thr Ala Asn Lys Val Val Asn Ser Ala Thr
210 215 220

Asn Thr Ser Ser Asn Val Thr His Asn Ala Val Asn Thr Ser Thr Ser
225 230 235 240

Ala Thr Cys Ser Tyr Gly Lys Val Ser Ala Arg Thr Arg Gly Asn Met
245 250 255

Ala Val Ser Thr Val Ser Ala Cys Ala Ala Gly Lys Ser Lys Val Gly
260 265 270

Ala Ser Thr Val Ser Ala Arg Val Met Tyr Asn Val Asn Gly Asn Asn
275 280 285

Thr Lys Asn His Gly Val Asn Tyr Ser Thr Ser Asn Asn Thr Tyr Cys
290 295 300

Asn Thr Asn Ser His Ser Ser Asn Asn Tyr Ser Ser Asp Ser Lys Lys
305 310 315 320

Asp His Thr Ser Ser Lys Tyr Asp His Asn His Asn Ala Lys Asn Lys
325 330 335

Gly Val Ser Asp Thr Asn Tyr Gly His Asn Ser Lys Val Lys Arg Lys
340 345 350

Asp Thr Asp Ala Lys Arg Arg Lys Asp Ser Asn Ser Ser Thr Met Ala
355 360 365

Val Met Asp Ser Ser Asp Tyr Gly Asn Thr Val Lys Asn Ser Ser Asn
370 375 380

Arg Asp Met Arg Lys Cys Asn Lys Tyr Thr Ser Met Gly Val His Lys
385 390 395 400

Asn Gly Thr Trp Val Cys Lys Lys Met Ala Asn Thr Arg Asn Val Thr
405 410 415

Ser Gly Val Ser Asp Tyr Cys Thr Asn Asp Gly Asn Tyr Val Gly Lys
420 425 430

Gly Trp Asn Ser Ser Val Ser His Trp Thr Val Asn Arg Tyr Gly Ser
435 440 445

Arg Ala Val Arg Ala Cys Ala Asp Ser Thr Cys Thr Thr Ser Val Ser
450 455 460

Tyr Ala Thr Asp Thr Asn Gly Thr Thr Trp Asp Thr Cys Thr Asn Lys
465 470 475 480

Asn Cys Asp Lys Val Asn Lys Asn Val Lys Cys Cys His Lys Gly Ser
485 490 495

Thr Cys Lys Asn Arg Gly Gly Ala Ser Lys Asn Lys His Ala Asp Gly
500 505 510

Ser Ser Asp Ser Asp Gly Asn Tyr Gly Thr Tyr Lys Val Thr Ser Arg
515 520 525

Asp Asn Ser Val Arg Asp Ala Thr Lys Arg Asn Ser Asn Asn Ser Arg
530 535 540

Val Gly Ser Ser Ala Gly Ser Lys Ser Ser Lys Asn His Gly Lys His
545 550 555 560

Gly His Ser Gly Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser
565 570 575

Ser Asn Ser Arg His Asn Ser Val Met Asn Asn Ala Gly Thr Ala Asn
580 585 590

Asn Ala Met Ser Asn Ser Tyr Asn Asn Val Val Tyr Ser Gly Asn Asn
595 600 605

Asn Asn Gly Asn Ser Asn Gly Asp Asn Ser Asp Ser Arg Ala Asn Gly
610 615 620

Thr Asn Ser Val Asn Asn Val Ser Asn Asn Asn Asn Asn Tyr Asn Asn
625 630 635 640

Ser Gly Tyr Ser Ser Met Asn Ser Arg Ser Val Ser His Asn Asn Asn
645 650 655

Asn Asn Thr Asn Asn Thr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn
660 665 670

Asn
675 680 685

Asn Ser Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asp Thr Ser Tyr Arg
690 695 700

Tyr Arg Ser Tyr Gly Tyr
705 710

<210> 34
<211> 477
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 34

Asp Thr Lys Gly Tyr Asp Asp Asp Ala Ala Thr Asp Gly Lys Lys His
1 5 10 15

Arg Arg Tyr Arg Tyr Val Ser Gly Ser Val Ser Gly Lys Arg Trp Thr
20 25 30

Asp Gly Val Ser Trp Ser Ser Arg Ser Gly Lys Tyr Lys Asp Lys Asn
35 40 45

Ala Gly Ser Asn Ala Asn Ala Thr Ser Ser Gly Ser Thr Asp Ser Ala
50 55 60

Val Thr Asp Gly Thr Ser Gly Ala Arg Asn Asn Ser Ser Ser Lys Lys
65 70 75 80

Lys Asn His Asp Thr Met Gly His Ser Ser Ser Asp Thr Ser Ser Ser
85 90 95

Asn Arg Ser Asn Lys Tyr Thr Gly Val Lys Lys Thr Ser Val Lys Lys
100 105 110

Arg Asn Ser Asn His Val Ser Tyr Tyr Ser Val Lys Asp Lys Asn Cys
115 120 125

Val Thr Lys Ala Ser Lys Asp Val Arg Ser Val Ala Met Gly Asn Thr
130 135 140

Thr Gly Asn Val Lys Asn Asn Ser Thr Thr Thr Gly Asn Gly Asn Asn
145 150 155 160

Asn Asn Lys Ser Asn Ser Ser Thr Asn Thr Val Ser Thr Asn Asn Asn
165 170 175

Ser Ala Asn Asn Ala Ala Gly Ser Asn Thr Ser Ala Asn Lys Asn Tyr
180 185 190

Tyr Tyr Lys Asn Asp Ser Ser Gly Tyr Thr Ala Ala Ser Thr Thr Met
195 200 205

Tyr Thr Ala Asn Tyr Thr Ser Asp Asn Thr Asn Ala Thr Gly Met Asn
210 215 220

Thr His Val Asn Asn Asn Asn Asn Ser Asn Asn Ser Ser Asn Ser
225 230 235 240

Asn Asn Ser Asn
245 250 255

Asn Asn Asn Asn Asn Asn Asn Val Asn Thr Asn Ala Gly Asn Gly
260 265 270

Asn Asn Asn Arg His Asn Ala Ser Ala Tyr Asn Thr Thr Gly Asp Asn
275 280 285

Gly Ser Tyr Tyr Tyr Thr Thr Asn Asn Asn Tyr Tyr Thr Thr Asn Val
290 295 300

Thr Asn Ala Ser Thr Asn Asn Gly Tyr Ser Thr Ser Ser Thr His Tyr
305 310 315 320

Tyr Gly His Thr Ser Ser Ala Ser Ala Ala Ala Gly Ala Thr Gly Thr
325 330 335

Gly Thr Ala Asn Val Val Ser Ser Met His Ala Asn Asn Asn Ser Ala
340 345 350

Ser Ser Ala Thr Ser Thr Ala Tyr Val Tyr Ser Met Asn Val Asn Val
355 360 365

Tyr Tyr Asn Ser Ser Ala Ser Ala Tyr Lys Arg Ala Asn Thr Thr Ser
370 375 380

Asn Thr Asn Ala Ser Gly Ala Thr Ser Thr Asn Ser Gly Thr Met Ser
385 390 395 400

Asn Ala Tyr Ala Asn Ser Tyr Thr Ser Val Tyr Tyr Gly Tyr Ala Met
405 410 415

Ala Ser Ala Asn Ser Met Tyr His His His Thr Val Tyr Ala Thr Asn
420 425 430

Met Ser Ser Gly His Thr Ser Thr Gly Ser Asp His His His Tyr Asn
435 440 445

Asp His Lys Asn Ala Met Gly His Ala Asn Asn Asn Asn Thr Asn Asn
450 455 460

Asp Thr Met Asn Asn Asn Thr Asn Thr Ser Thr Thr Thr
465 470 475

<210> 35
<211> 454
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 35

Met Asp Val Arg Ala Ala Cys Ser Ala Ser Gly Arg Thr Gly Lys Lys
1 5 10 15

Gly Tyr Ser Tyr Lys Met Ser Asn Ser Gly Gly Ser Ser Ser Gly Gly
20 25 30

Ser Asp Val Gly Ser Thr Asn Gly Ser Asn Arg Ala Lys Asn Thr Asn
35 40 45

Tyr Lys Lys Thr Asn Lys Lys Tyr Lys Ala Thr Asp Lys Ala Asn Asp
50 55 60

Thr Lys Tyr Tyr Ser Asn Asp Lys Lys Ser Lys Arg Ser Ala Asn Ser
65 70 75 80

Met Asn Asp Lys Asp Lys Cys Arg Thr Thr Asn Lys Asp Met Thr Arg
85 90 95

Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser
100 105 110

His Ser Met Lys Tyr Lys Lys Arg Ser Val Asp Lys Asp His Val Met
115 120 125

Lys Asp Asp Ser Ser Val Lys Ala Ser Lys Met Asn Ser His Asn Tyr
130 135 140

Ser Thr Asn Thr Met Asn Lys Met Asp Val Tyr Thr Lys Ala Asn Met
145 150 155 160

Ala Asn Lys Lys Lys Ser Asp Thr Ser Thr Trp Lys Asn Lys Asn Lys
165 170 175

Ser His Val Ser Tyr Asn Asn Asp Lys Ser Lys Thr Lys Trp Tyr Asn
180 185 190

Asp Ser Asp Asp Asp Asp Asn Asn Val Asn Asn Asn Asp Asn Asn
195 200 205

Asn Asn Asn Lys Asn Asp Asn Asn Asn Asp Asn Asn Asn Asp Thr Ser
210 215 220

Asn Asn Asn Asn Asn Asn Asn Arg Thr Lys Asn Asn Arg Asn Asn
225 230 235 240

Arg Asp Trp Lys Thr Lys Lys Cys Thr Asp Met Asn Asp Lys Arg Asp
245 250 255

Asn Asn Asn Lys Asn Asp Met Ala Arg Asn Asp Asn Lys Asn Tyr Asn
260 265 270

Asn Val Asn Lys Arg Asn His Lys Ser Ser Cys Arg Arg Asp Gly Tyr
275 280 285

Ser Ala Asn Asn Ala Val Asn Ser Thr His Ala Ser Asn Lys Asn Val
290 295 300

Asn Asp Met Asn Asn Asp Thr Tyr Lys Asn Lys Thr Asp Thr Asn Lys
305 310 315 320

Lys Asn Asp Ser Asn Ser Asp Val Thr Arg Lys Lys Arg Lys Thr
325 330 335

Ser Asp Gly Asn Tyr Ser Arg Asn Asn Val Ser Val Ser Arg Ser Lys
340 345 350

Ala Thr Thr Lys Lys Thr Lys Lys Lys Arg Arg Asp Gly Lys Asp
355 360 365

Lys Lys Asn Lys Lys Asn Ala Asp Asn Lys Lys Asn Asn Ala Val Thr
370 375 380

Val Ser Val Tyr Asp Ser Asn Lys Val Lys Ser Asn Lys Arg Ser Arg
385 390 395 400

Lys Val Asn Asn Lys Ser Asp Val Val Asn Ser Gly Lys Asp Ser Arg
405 410 415

Val Lys Ser Cys Lys Lys Tyr Ala Asp Asn Asn Thr Lys Ser Asn Asp
420 425 430

Ala Asp Gly Trp Asp Asp Met Asn Trp Val Asp Arg Gly Cys Ala Thr
435 440 445

Thr Arg Trp Arg Ala Lys
450

<210> 36
<211> 284
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 36

Met Asn Val Thr Ser Lys Asp Gly Asn His Ser Ser Lys Lys Asn Arg
1 5 10 15

Asn Thr Asn Lys Arg His Lys Asn Ala Ser Asn Asp Arg Asp Ser Val
20 25 30

Ser Ser Asn Thr Thr Ser Met Thr Asp Asp Ala Asp Tyr Asn Gly Ala
35 40 45

Ser Arg Thr Lys Asn Asn Ser Asp Ser Asp Arg Ser Asn Asp Thr Lys
50 55 60

Asn Asn Tyr Asn Lys Arg Thr Gly Tyr Asn Tyr Asn Gly Ser Gly Asn
65 70 75 80

Arg Tyr Thr Arg Lys Arg Thr Ala Asn Lys Ala Tyr Ser Asp Asp Asn
85 90 95

Val Lys Asp Asp Asn Asn Thr Lys Lys Ala Ser Arg Ser Ser Gly Arg
100 105 110

Asn Val Asn Thr Arg Asn Lys Ser Lys Ser His Lys Val Lys Asn Asn
115 120 125

Lys Ser Ser Ser Arg Lys Ser Ser Ala Ala Arg Lys Gly Lys Tyr Asn
130 135 140

Ser Asn Ser Asp Ser Thr Thr Arg Lys Val Thr Asp Val Lys Lys Arg
145 150 155 160

Ser Lys Trp His Arg His Asp Lys Lys Met Val Lys Lys Ser Arg Tyr
165 170 175

Arg Lys Arg Met Arg Gly Thr Asp Val Ser Ser Asp Asn Ser Lys
180 185 190

Ser Thr Thr Lys Ser Tyr Val Ser Lys Asn Ser Ala Met Asn Asn Asn
195 200 205

Asp Val Thr Asp Asn Lys Lys Thr Asn Asn Asn Lys Ala Arg Asp Ser
210 215 220

Met His Thr Lys Lys Asp Thr Lys Asp Asp Thr Asp Ser Lys Lys Arg
225 230 235 240

Lys Val Val Thr Asn Asp Asn Ala Ala Met Val Asn Lys Gly Trp Arg
245 250 255

Lys Asn Val Met Met Tyr Lys Lys Ser Gly Asn Met Lys Lys Tyr Arg
260 265 270

Tyr Trp Thr Cys Tyr Cys Asn Tyr Val Tyr Tyr Arg
 275 280

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic primer

<400> 37
 gggaaattcccc attaccgaca tttggggcgc 29

<210> 38
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic primer

<400> 38
 ggggattctg attgatttgat tgattgtac 29

<210> 39
 <211> 720
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Superbright GFP encoding sequence

<220>
 <221> CDS
 <222> (1)..(720)

<400> 39
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 96
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 144
 35 40 45

tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 192
 50 55 60

ttc act tat ggt gtt cag tgc ttt tca aga tac ccg gat cat atg aaa
 Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 240
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
aga act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
att gat ttt aaa gaa gat gga aac att ctt ggg cac aaa ttg gaa tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
gga atc aaa gct aac ttc aaa att aga cac aac att gaa gat gga agc			528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc			576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn thr Pro Ile Gly Asp gly			
180	185	190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt			624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu glu Phe			
210	215	220	
gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga			720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp glu Leu Tyr Lys			
225	230	235	240

<210> 40
 <211> 239
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Peptide

<400> 40

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

55

60

Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 41

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 41

gaccgcggat ggctagcaaa ggagaag

27

<210> 42

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 42
cctgagctct catttgtata gttcatcc

28

<210> 43
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 43
ggaggatcca tggatacggta taagtttaatc tcag

34

<210> 44
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 44
ggaccgcggg tagcgggtct gttgagaaaa gttgcc

36

<210> 45
<211> 7239
<212> DNA
<213> Artificial sequence

<220>
<223> Vector containing chimeric gene

<400> 45
gacgaaaggg cctcggtata cgcctatttt tataggtaa tgtcatgata ataatggttt 60
cttaggacgg atcgcttgcc tctaacttac acgcgcctcg tatcttttaa tggatggata 120
atttggaaat ttactctgtg tttatatttt tttatgtttt gtatggat ttttagaaagt 180
aaataaaagaa ggttagaagag ttacgaaatg aaaaaaaaaa aataaacaaa ggtttaaaaa 240
atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata 300
gatatacatt cgattaacga taagtaaaat gtaaaatcac aggatttcg tgtgtggct 360
tctcacacaga caagatgaaa caattcggca ttaatacctg agagcaggaa gagcaagata 420
aaaggttagta tttgttggcg atccccctag agtctttac atcttcggaa aacaaaaact 480
atttttctt taatttcttt ttttacttcc tatttttaat ttatataattt atattaaaaa 540
atttaaatttta taatttatttt tatagcacgt gatgaaaagg acccaggtgg cactttcgg 600
ggaaatgtgc gcggaaacccc tatttgttta ttttctaaa tacattcaaa tatgtatccg 660
ctcatgagac aataaccctg ataaatgctt caataatattt gaaaaaggaa gagttatgagt 720

attcaacatt	tccgtgtcgc	ccttattccc	tttttgcgg	cattttgcct	tcctgtttt	780
gctcacccag	aaacgctgg	gaaagtaaaa	gatgctgaag	atcagttggg	tgcacgagtg	840
ggttacatcg	aactggatct	caacagcggt	aagatccttgc	agagtttcg	ccccgaagaa	900
cgtttccaa	tgatgagcac	ttttaaagtt	ctgctatgtg	gcgcggtatt	atcccgtatt	960
gacgcccggc	aagagcaact	cggtcgccgc	atacactatt	ctcagaatga	cttgggttag	1020
tactcaccag	tcacagaaaa	gcatcttacg	gatggcatga	cagtaagaga	attatgcagt	1080
gctgccataa	ccatgagtga	taacactgcg	gccaaacttac	ttctgacaac	gatcggagga	1140
ccgaaggagc	taaccgc	tttgcacaac	atgggggatc	atgtaactcg	ccttgatcgt	1200
tggaaaccgg	agctgaatga	agccatacca	aacgacgagc	gtgacaccac	gatgcctgta	1260
gcaatggcaa	caacgttgcg	caaactatta	actggcgaac	tacttactct	agcttcccg	1320
caacaattaa	tagactggat	ggaggcggat	aaagttgcag	gaccacttct	gcgctcgcc	1380
cttccggctg	gctggtttat	tgctgataaa	tctggagccg	gtgagcgtgg	gtctcgccgt	1440
atcattgcag	cactggggcc	agatggtaag	ccctcccgta	tcgtagttat	ctacacgacg	1500
gggagtcagg	caactatgga	tgaacgaaat	agacagatcg	ctgagatagg	tgccctactg	1560
attaagcatt	ggtaactgtc	agaccaagtt	tactcatata	tactttagat	tgatttaaaa	1620
cttcattttt	aatttaaaag	gatctaggtg	aagatcctt	ttgataatct	catgaccaaa	1680
atcccttaac	gtgagtttc	gttccactga	gcgtcagacc	ccgtagaaaa	gatcaaagga	1740
tcttctttag	atcctttttt	tctgcgcgta	atctgctgct	tgcaaacaaa	aaaaccaccc	1800
ctaccagcgg	tggttgttt	gccggatcaa	gagctaccaa	ctcttttcc	gaaggtaact	1860
ggcttcagca	gagcgcagat	accaaatact	gtccttctag	tgtagccgta	gttaggccc	1920
cacttcaaga	actctgttagc	accgcctaca	tacctcgctc	tgctaattct	gttaccagtg	1980
gctgctgcca	gtggcgataa	gtcgtgtctt	accgggttgg	actcaagacg	atagttaccc	2040
gataaggcgc	agcggtcggg	ctgaacgggg	ggtcgtgca	cacagcccag	cttggagcga	2100
acgacctaca	ccgaactgag	atacctacag	cgtgagctat	gagaaagcgc	cacgcttccc	2160
gaagggagaa	aggcggacag	gtatccggt	agcggcaggg	tcggaacagg	agagcgcacg	2220
agggagcttc	cagggggaaa	cgcctggat	ctttagatgc	ctgtcgggtt	tcgcccaccc	2280
tgacttgagc	gtcgattttt	gtgatgctcg	tcaggggggc	ggagccatag	aaaaaacgcc	2340
agcaacgcgg	ccttttacg	gttcctggcc	ttttgctggc	cttttgcctca	catgttctt	2400
cctgcgttat	cccctgattc	tgtggataac	cgtattaccg	cctttgagtg	agctgataacc	2460
gctcgccgca	gccgaacgac	cgagcgcagc	gagtcagtga	gcgaggaagc	ggaagagcgc	2520
ccaatacgca	aaccgcctct	ccccgcgcgt	tggccgattc	attaatgcag	ctggcacgac	2580
aggttcccg	actggaaagc	gggcagttag	cgcaacgcaa	ttaatgttag	ttacctcact	2640

cattaggcac cccaggctt acactttatg cttccggctc gtagtggatg tgaaattgtg	2700
agcgataac aatttcacac aggaaacagc tatgaccatg attacgcca gctcgaaatt	2760
aaccctcact aaagggaca aagctgggt accggggccc ccctcgaggt cgacggtac	2820
gataagctt atatcgatt cccattaccg acatttgggc gctatacgtg catatgttca	2880
tgtatgtatc tgtatattaaa acactttgtt attattttc ctcataatgt tgtataggtt	2940
tatacggatg attaattat tacttcacca ccctttattt caggctgata tcttagcctt	3000
gttacttagt agaaaaagac attttgctg tcagtcactg tcaagagatt ctggctgg	3060
cattttcttct agaagcaaaa agagcgatgc gtctttccg ctgaaccgtt ccagcaaaaa	3120
agactaccaa cgcaatatgg attgtcagaa tcatataaaa gagaagcaaa taactccttgc	3180
tcttgtatca attgcattat aatatcttct tggtagtgca atatcatata gaagtcatcg	3240
aaatagatataa taagaaaaac aaactgtaca atcaatcaat caatcaggat ccatggatac	3300
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 <212> PRT
 <213> *Pichia pinus*

<400> 46

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Ala Val Gln Ser Tyr Ile Pro Asn Thr Ala Gln Ala Phe Val Pro Ser
 35 40 45

Ala Gln Pro Tyr Ile Pro Gly Gln Gln Glu Gln Gln Phe Gly Gln Tyr
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Gly Gln Gln Gln Gln Asn Tyr Asn Gln Gly Gly Tyr Asn Asn Tyr Asn
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Asn Arg Gly Gly Tyr Ser Asn Asn Arg Gly Gly Tyr Asn Asn Ser Asn
 85 90 95

Arg Gly Gly Tyr Ser Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Asn Gln
 100 105 110

Gly Gly Tyr Ser Asn Tyr Asn Asn Tyr Ala Asn Asn Ser Tyr Asn

115

120

125

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Asn Ser Gln Pro Gln Gly Gln Asp Gln Gln Gln Glu Thr Gly Ser Gly
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Gln Met Ser Leu Glu Asp Tyr Gln Lys Gln Gln Lys Glu Ser Leu Asn
165 170 175

Lys Leu Asn Thr Lys Pro Lys Lys Val Leu Lys Leu Asn Leu Asn Ser
180 185 190

Ser Thr Val Lys Ala Pro Ile Val Thr Lys Lys Lys Glu Glu Glu Pro
195 200 205

Val Asn Gln Glu Ser Lys Thr Glu Glu Pro Ala Lys Glu Glu Ile Lys
210 215 220

Asn Gln Glu Pro Ala Glu Ala Glu Asn Lys Val Glu Glu Glu Ser Lys
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Val Glu Ala Pro Thr Ala Ala Lys Pro Val Ser Glu Ser Glu Phe Pro
245 250 255

Ala Ser Thr Pro Lys Thr Glu Ala Lys Ala Ser Lys Glu Val Ala Ala
260 265 270

Ala Ala Ala Ala Leu Lys Lys Glu Val Ser Gln Ala Lys Lys Glu Ser
275 280 285

Asn Val Thr Asn Ala Asp Ala Leu Val Lys Glu Gln Glu Glu Gln Ile
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Asp Ala Ser Ile Val Asn Asp Met Phe Gly Gly Lys Asp His Met Ser
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Ile Ile Phe Met Gly His Val Asp Ala Gly Lys Ser Thr Met Gly Gly
325 330 335

Asn Leu Leu Phe Leu Thr Gly Ala Val Asp Lys Arg Thr Val Glu Lys
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Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg Gln Gly Trp Tyr Leu Ser
355 360 365

Trp Ile Met Asp Thr Asn Lys Glu Glu Arg Asn Asp Gly Lys Thr Ile
370 375 380

Glu Val Gly Lys Ser Tyr Phe Glu Thr Asp Lys Arg Arg Tyr Thr Ile
385 390 395 400

Leu Asp Ala Pro Gly His Lys Leu Tyr Ile Ser Glu Met Ile Gly Gly
405 410 415

Ala Ser Gln Ala Asp Val Gly Val Leu Val Ile Ser Ser Arg Lys Gly
420 425 430

Glu Tyr Glu Ala Gly Phe Glu Arg Gly Gly Gln Ser Arg Glu His Ala
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Ile Leu Ala Lys Thr Gln Gly Val Asn Lys Leu Val Val Val Ile Asn
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Cys Thr Thr Lys Leu Ala Met Tyr Leu Lys Gly Val Gly Tyr Gln Lys
485 490 495

Gly Asp Val Leu Phe Met Pro Val Ser Gly Tyr Thr Gly Ala Gly Leu
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530 535 540

Asp Pro Phe Met Leu Pro Ile Ser Ser Lys Met Lys Asp Leu Gly Thr
545 550 555 560

Val Ile Glu Gly Lys Ile Glu Ser Gly His Val Lys Lys Gly Gln Asn
565 570 575

Leu Leu Val Met Pro Asn Lys Thr Gln Val Glu Val Thr Thr Ile Tyr
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Asn Glu Thr Glu Ala Glu Ala Asp Ser Ala Phe Cys Gly Glu Gln Val
595 600 605

Arg Leu Arg Leu Arg Gly Ile Glu Glu Glu Asp Leu Ser Ala Gly Tyr
610 615 620

Val Leu Ser Ser Ile Asn His Pro Val Lys Thr Val Thr Arg Phe Glu
625 630 635 640

Ala Gln Ile Ala Ile Val Glu Leu Lys Ser Ile Leu Ser Thr Gly Phe
645 650 655

Ser Cys Val Met His Val His Thr Ala Ile Glu Glu Val Thr Phe Thr
660 665 670

Gln Leu Leu His Asn Leu Gln Lys Gly Thr Asn Arg Arg Ser Lys Lys
675 680 685

Ala Pro Ala Phe Ala Lys Gln Gly Met Lys Ile Ile Ala Val Leu Glu
690 695 700

Thr Thr Glu Pro Val Cys Ile Glu Ser Tyr Asp Asp Tyr Pro Gln Leu
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Val Thr Lys Leu Leu
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<212> PRT
<213> Candida albicans

<400> 47

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Ala Gln Ser Phe Val Pro Gln Gly Gly Tyr Gln Gln Phe Gln Gln Phe
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Gln Pro Gln Gln Gln Gln Gln Tyr Gly Gly Tyr Asn Gln Tyr Asn
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Gln Tyr Gln Gly Gly Tyr Gln Gln Asn Tyr Asn Asn Arg Gly Gly Tyr
65 70 75 80

Gln Gln Gly Tyr Asn Asn Arg Gly Gly Tyr Gln Gln Asn Tyr Asn Asn
85 90 95

Arg Gly Gly Tyr Gln Gly Tyr Asn Gln Asn Gln Gln Tyr Gly Gly Tyr
100 105 110

Gln Gln Tyr Asn Ser Gln Pro Gln Gln Gln Gln Gln Ser Gln
115 120 125

Gly Met Ser Leu Ala Asp Phe Gln Lys Gln Lys Thr Glu Gln Gln Ala
130 135 140

Ser Leu Asn Lys Pro Ala Val Lys Lys Thr Leu Lys Leu Ala Gly Ser
145 150 155 160

Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Asp Thr Thr Ser
165 170 175

Lys Pro Gln Ser Lys Glu Ser Ser Pro Ala Pro Ala Pro Ala Ala Ser
180 185 190

Ala Ser Ala Ser Ala Pro Gln Glu Glu Lys Lys Glu Glu Lys Glu Ala
195 200 205

Ala Ala Ala Thr Pro Ala Ala Ala Pro Glu Thr Lys Lys Glu Thr Ser
210 215 220

Ala Pro Ala Glu Thr Lys Lys Glu Ala Thr Pro Thr Pro Ala Ala Lys
225 230 235 240

Asn Glu Ser Thr Pro Ile Pro Ala Ala Ala Lys Lys Glu Ser Thr
245 250 255

Pro Cys Ser Asn Ser Ala Ser Val Ala Thr Ala Asp Ala Leu Val Lys
260 265 270

Glu Gln Glu Asp Glu Ile Asp Glu Glu Val Val Lys Asp Met Phe Gly
275 280 285

Gly Lys Asp His Val Ser Ile Ile Phe Met Gly His Val Asp Ala Gly
290 295 300

Lys Ser Thr Met Gly Gly Asn Ile Leu Tyr Leu Thr Gly Ser Val Asp
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Lys Arg Thr Val Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
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Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
340 345 350

Asn Asp Gly Leu Thr Ile Glu Val Gly Lys Ala Tyr Phe Glu Thr Asp
355 360 365

Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly His Lys Met Tyr Val
370 375 380

Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Ile Leu Val
385 390 395 400

Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Lys Gly Gly
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Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
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Ile Ile Val Val Val Asn Lys Met Asp Asp Ser Thr Val Gly Trp Ser
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Lys Glu Arg Tyr Gln Glu Cys Thr Thr Lys Leu Gly Ala Phe Leu Lys
450 455 460

Gly Ile Gly Tyr Ala Lys Asp Asp Ile Ile Tyr Met Pro Val Ser Gly
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Tyr Thr Gly Ala Gly Leu Lys Asp Arg Val Asp Pro Lys Asp Cys Pro
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Trp Tyr Asp Gly Pro Ser Leu Leu Glu Tyr Leu Asp Asn Met Asp Thr
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Met Asn Arg Lys Ile Asn Gly Pro Phe Met Met Pro Val Ser Gly Lys
515 520 525

Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly His
530 535 540

Val Lys Lys Gly Thr Asn Leu Ile Met Met Pro Asn Lys Thr Pro Ile
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Glu Val Leu Thr Ile Phe Asn Glu Thr Glu Gln Glu Cys Asp Thr Ala
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Phe Ser Gly Glu Gln Val Arg Leu Lys Ile Lys Gly Ile Glu Glu Glu
580 585 590

Asp Leu Gln Pro Gly Tyr Val Leu Thr Ser Pro Lys Asn Pro Val Lys
595 600 605

Thr Val Thr Arg Phe Glu Ala Gln Ile Ala Ile Val Glu Leu Lys Ser
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Ile Leu Ser Asn Gly Phe Ser Cys Val Met His Leu His Thr Ala Ile
625 630 635 640

Glu Glu Val Lys Phe Ile Glu Leu Lys His Lys Leu Glu Lys Gly Thr
645 650 655

Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met Lys
660 665 670

Ile Ile Ala Ile Leu Glu Val Gly Glu Leu Val Cys Ala Glu Thr Tyr
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<220>

<223> Ure2N-Sup35C integration plasmid

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tgtgcacgaa ccccccgttc agcccgaccg ctgcgcctta tccggtaact atcgtcttga	6480
gtccaacccg gtaagacacg acttatcgcc actggcagca gccactggta acaggattag	6540
cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tggtggccta actacggcta	6600
cactagaagg acagtatttg gatatcgcc tctgctgaag ccagttaccc tcggaaaaag	6660
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agaatagtgt atgcggcgac cgagttgctc ttgccccggcg tcaatacggg ataataccgc	7560

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ctttcgtc 7988

<210> 50
<211> 405
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 50

Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
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Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
20 25 30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
35 40 45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
50 55 60

Gln Asp Arg Ala Ala Gly Gly Ser Ser Phe Met Asn Thr Leu Met
65 70 75 80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
85 90 95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
100 105 110

Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
115 120 125

Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
130 135 140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
145 150 155 160

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
165 170 175

Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
180 185 190

Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
195 200 205

Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
210 215 220

Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225 230 235 240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
245 250 255

Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
260 265 270

Met Ala Gln Ser Tyr Leu Gly Gly Gln Tyr Gln Ser Asn Gln Gln
275 280 285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
290 295 300

Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gln Gly
305 310 315 320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
325 330 335

Gly Asn Asn Ser Asn Ser Asn Ser Tyr Gly Gly Gln Gln Gln Ala
340 345 350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Ser Asn Glu
355 360 365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
370 375 380

Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
385 390 395 400

Asn Gln Asn Arg Tyr
405

<210> 51
<211> 128
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 51

Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Glu Lys Ser Gln
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Tyr Ser Arg Pro Ser Asn Pro Pro Pro Ser Ser Ala His Gln Asn Lys
20 25 30

Thr Gln Glu Arg Gly Tyr Pro Pro Gln Gln Gln Gln Tyr Tyr Gln
35 40 45

Gln Gln Gln Gln His Pro Gly Tyr Tyr Asn Gln Gln Gly Tyr Asn Gln
50 55 60

Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln
65 70 75 80

Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly His Gln Gln Pro Val
85 90 95

Tyr Val Gln Gln Pro Pro Gln Arg Gly Asn Glu Gly Cys Leu Ala
100 105 110

Ala Cys Leu Ala Ala Leu Cys Ile Cys Cys Thr Met Asp Met Leu Phe
115 120 125

<210> 52
<211> 534
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 52

Met Ser Ser Asp Glu Glu Asp Phe Asn Asp Ile Tyr Gly Asp Asp Lys
1 5 10 15

Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Gln Asn Lys Ala
20 25 30

Gly Ser Gly Thr Ser Gln Leu Asp Gln Leu Ala Ala Leu Gln Ala Leu
35 40 45

Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
50 55 60

Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr

65

70

75

80

Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
85 90 95

Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Ser Ser Ala
100 105 110

Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln
115 120 125

Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Gln Gln Gln Val Thr Gln
130 135 140

Thr Lys Glu Glu Arg Ser Lys Ala Asp Leu Ser Lys Glu Ser Cys Lys
145 150 155 160

Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Leu Arg
165 170 175

Glu Tyr Phe Gly Lys Tyr Gly Thr Val Thr Asp Leu Lys Ile Met Lys
180 185 190

Asp Pro Ala Thr Gly Arg Ser Arg Gly Phe Gly Phe Leu Ser Phe Glu
195 200 205

Lys Pro Ser Ser Val Asp Glu Val Val Lys Thr Gln His Ile Leu Asp
210 215 220

Gly Lys Val Ile Asp Pro Lys Arg Ala Ile Pro Arg Asp Glu Gln Asp
225 230 235 240

Lys Thr Gly Lys Ile Phe Val Gly Ile Gly Pro Asp Val Arg Pro
245 250 255

Lys Glu Phe Glu Glu Phe Ser Gln Trp Gly Thr Ile Ile Asp Ala
260 265 270

Gln Leu Met Leu Asp Lys Asp Thr Gly Gln Ser Arg Gly Phe Gly Phe
275 280 285

Val Thr Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Gln Asn Lys
290 295 300

Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro
305 310 315 320

Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly
325 330 335

Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe
340 345 350

Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met
355 360 365

Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr
370 375 380

Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Gln
385 390 395 400

Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro
405 410 415

Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr
420 425 430

Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp
435 440 445

Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro
450 455 460

Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
465 470 475 480

His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
485 490 495

Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
500 505 510

Arg Asn Gly Arg Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
515 520 525

Tyr His Pro Tyr Asn Arg
530

<210> 53
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 53		
ggaggatcca tggatacggtaa	tcag	34
<210> 54		
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<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic primer		
<400> 54		
ccaagcttccatagcggtt	ctgttgagaa aagttg	36
<210> 55		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic primer		
<400> 55		
ggtgtcttgg	ccaattgccc	20
<210> 56		
<211> 39		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic primer		
<400> 56		
gtcgacacctgc	agcgtacgca tttcagatct ttgtatac	39
<210> 57		
<211> 40		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic primer		
<400> 57		
cgagctcgaa	ttcatcgatt gattcagttc gccttctatac	40
<210> 58		
<211> 22		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Synthetic primer		
<400> 58		
ctgtttgaa	agggtccaca tg	22

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<210> 59
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 59
ggaggatcca tggatacgga taagttaatc tcag 34

<210> 60
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 60
ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

<210> 61
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 61
gaggatccat gcctgatgat gaggaagaag acgagg 36

<210> 62
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 62
cgaaattcct cgagaagata tccatc 26

<210> 63
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 63
gggatcctgt tgcttagtggg caga 24

<210> 64
<211> 34
<212> DNA

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<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 64

gtaccgcgga tgtctttgaa cgactttcaa aagc

34

<210> 65

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 65

gtggagctct tactcgccaa ttttaacaat tttac

35

<210> 66

<211> 3153

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 66

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60

aaccaacaac aaggtaacaa cagataccaa ggttatcaag cttacaatgc tcaagccaa

120

cctgcaggtg ggtactacca aaattaccaa ggttattctg ggtaccaaca aggtggctat

180

caacagtaca atcccgacgc cggttaccag caacagtata atcctaagg aggctatcaa

240

cagtacaatc ctcaaggcgg ttatcagcag caattcaatc cacaagggtgg ccgtggaaat

300

tacaaaaact tcaactacaa taacaatttgc aaggatatc aagctggttt ccaaccacag

360

tctcaaggta tgtctttgaa cgactttcaa aagcaacaaa agcaggccgc tcccaaacca

420

aagaagactt tgaagcttgt ctccagttcc ggtatcaagt tggccaatgc taccaagaag

480

gttggcacaa aacctgcccga atctgataag aaagaggaag agaagtctgc taaaaccaaa

540

gaaccaacta aagagccaac aaaggtcgaa gaaccagtta aaaaggagga gaaaccagtc

600

cagactgaag aaaagacgga ggaaaaatcg gaacttccaa aggtagaaga cttaaaatc

660

tctgaatcaa cacataatac caacaatgcc aatgttacca gtgtgtatgc cttgtatcaag

720

gaacaggaag aagaagtggc tgacgaagtt gttaacgatc cgcggatggc ctccaaagaa

780

tccttagctc cccctggtag agacgaagtc cctggcagtt tgcttggcca agggaggggg

840

agcgtaatgg actttataa aagcctgagg ggaggagcta cagtcaaggt ttctgcattct

900

tcgcctcag tggctgctgc ttctcaggca gattccaagc agcagaggat tctccttgat

960

ttctcgaaag gctccacaag caatgtgcag cagcgacagc agcagcagca gcagcagcag

1020

cagcagcagc agcagcagca gcagcagcag cagccaggct tatccaaagc cgtttcactg

1080

tccatggggc tgtatatggg agagacagaa acaaaagtga tggggaatga cttgggctac	1140
ccacagcagg gccaacctgg ctttcctct gggaaacag acttcggct tctgaaagaa	1200
agcattgcaa acctcaatag gtcgaccagc gttccagaga accccaaagag ttcaacgtct	1260
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tcagaacagc aaaatcgaaa aagccagacc ggcaccaacg gaggcagtgt gaaattgtat	1380
cccacagacc aaagcacctt tgacctctt aaggatttg agtttccgc tgggtccca	1440
agtaaagaca caaacgagag tccctggaga tcagatctgt tgatagatga aaacttgctt	1500
tctccttgg cgggagaaga tgatccattc cttctcgaa ggaacacgaa tgaggattgt	1560
aagcctctta ttttaccgga cactaaacct aaaattaagg atactggaga tacaatctta	1620
tcaagtccca gcagtgtggc actacccaa gtaaaaacag aaaaagatga tttcattgaa	1680
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acctctggag gacagatgta ccactatgac atgaatacag catcccttc tcagcagcag	1860
gatcagaagc ctgttttaa tgtcattcca ccaattcctg ttggctctga aaactggaat	1920
aggtgccaag gctccggaga ggacagcctg acttccttg gggctctgaa cttcccaggc	1980
cggtcagtgt tttctaattgg gtactcaagc cctgaaatga gaccagatgt aagctctcct	2040
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ctcaccccta cttgggtgtc actgctggag gtgattgaac ccgaggtgtt gtatgcagga	2460
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attattaatg agcagagaat gtctctaccc tgcattgtatg accaatgtaa acacatgctg	2760
tttgcctcct ctgaattaca aagaatgcag gtatcctatg aagagtatct ctgtatgaaa	2820
accttactgc ttctctcctc agttcctaag gaaggtctga agagccaaga gttatttgat	2880
gagattcgaa tgacttataat caaagagcta ggaaagcca tcgtcaaaag ggaagggAAC	2940
tccagtcaga actggcaacg gttttaccaa ctgacaaagc ttctggactc catgcattgag	3000

gtggttgaga atcccttac ctactgcttc cagacatttt tggataagac catgagtatt 3060
gaattccag agatgttagc taaaatcatc actaatcaga taccaaaata ttcaaattgga 3120
aatatcaaaa agcttctgtt tcatcaaaaa tga 3153

<210> 67
<211> 1052
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 67

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15

Ser Gln Asn Gly Asn Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30

Gln Ala Tyr Asn Ala Gln Ala Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
50 55 60

Pro Asp Ala Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
65 70 75 80

Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Phe Asn Pro Gln Gly
85 90 95

Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
100 105 110

Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
115 120 125

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
130 135 140

Lys Leu Val Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
145 150 155 160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
165 170 175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
180 185 190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu

195

200

205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
210 215 220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225 230 235 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Pro Arg Met
245 250 255

Asp Ser Lys Glu Ser Leu Ala Pro Pro Gly Arg Asp Glu Val Pro Gly
260 265 270

Ser Leu Leu Gly Gln Gly Arg Gly Ser Val Met Asp Phe Tyr Lys Ser
275 280 285

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Val
290 295 300

Ala Ala Ala Ser Gln Ala Asp Ser Lys Gln Gln Arg Ile Leu Leu Asp
305 310 315 320

Phe Ser Lys Gly Ser Thr Ser Asn Val Gln Gln Arg Gln Gln Gln
325 330 335

Gln Pro
340 345 350

Gly Leu Ser Lys Ala Val Ser Leu Ser Met Gly Lys Tyr Met Gly Glu
355 360 365

Thr Glu Thr Lys Val Met Gly Asn Asp Leu Gly Tyr Pro Gln Gln Gly
370 375 380

Gln Leu Gly Leu Ser Ser Gly Glu Thr Asp Phe Arg Leu Leu Glu Glu
385 390 395 400

Ser Ile Ala Asn Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys
405 410 415

Ser Ser Thr Ser Ala Thr Gly Cys Ala Thr Pro Thr Glu Lys Glu Phe
420 425 430

Pro Lys Thr His Ser Asp Ala Ser Ser Glu Gln Gln Asn Arg Lys Ser
435 440 445

Gln Thr Gly Thr Asn Gly Gly Ser Val Lys Leu Tyr Pro Thr Asp Gln
450 455 460

Ser Thr Phe Asp Leu Leu Lys Asp Leu Glu Phe Ser Ala Gly Ser Pro
465 470 475 480

Ala Ser Lys Asp Thr Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile
485 490 495

Asp Glu Asn Leu Leu Ser Pro Leu Ala Gly Glu Asp Asp Pro Phe Leu
500 505 510

Leu Glu Gly Asn Thr Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp
515 520 525

Thr Lys Pro Lys Ile Lys Asp Thr Gly Asp Thr Ile Leu Ser Ser Pro
530 535 540

Ser Ser Val Ala Leu Pro Gln Val Lys Thr Glu Lys Asp Asp Phe Ile
545 550 555 560

Glu Leu Cys Thr Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Pro Val
565 570 575

Tyr Cys Gln Ala Ser Phe Ser Gly Thr Asn Ile Ile Gly Asn Lys Met
580 585 590

Ser Ala Ile Ser Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr
595 600 605

His Tyr Asp Met Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys
610 615 620

Pro Val Phe Asn Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp
625 630 635 640

Asn Arg Cys Gln Gly Ser Gly Glu Asp Ser Leu Thr Ser Leu Gly Ala
645 650 655

Leu Asn Phe Pro Gly Arg Ser Val Phe Ser Asn Gly Tyr Ser Ser Pro
660 665 670

Gly Met Arg Pro Asp Val Ser Ser Pro Pro Ser Ser Ser Ala Ala
675 680 685

Thr Gly Pro Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser
690 695 700

Gly Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe
705 710 715 720

Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn
725 730 735

Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg
740 745 750

Tyr Arg Lys Cys Leu Gln Ala Gly Met Ala Asn Leu Glu Ala Arg Lys
755 760 765

Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
770 775 780

Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
785 790 795 800

Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro
805 810 815

Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp
820 825 830

Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala
835 840 845

Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu
850 855 860

Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala
865 870 875 880

Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu
885 890 895

Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro
900 905 910

Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu
915 920 925

Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu
930 935 940

Leu Leu Leu Ser Ser Val Pro Lys Glu Gly Leu Lys Ser Gln Glu Leu
945 950 955 960

Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile
965 970 975

Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln
980 985 990

Leu Thr Lys Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu
995 1000 1005

Thr Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu
1010 1015 1020

Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys
1025 1030 1035

Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln Lys
1040 1045 1050

<210> 68
<211> 158
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 68

Met Ser Thr Val Pro Leu Val Tyr Ser Pro Val Asp Arg Glu Pro Leu
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His Asp Asn Ser Ala Asn Ile Lys Arg Pro Leu Gly Ser Phe Val Thr
20 25 30

Ser Ser Ala Ala Cys Phe Lys Pro Leu Thr Ile Pro Gly Pro Thr Thr
35 40 45

Pro Cys Ala Phe Val Met Ser Ala His Ser Ala Ile Leu Tyr Thr Pro
50 55 60

Ala Glu Tyr Cys Asn Leu Thr Val Leu Pro Met Ser Ala Asn Phe Leu
65 70 75 80

Ser Ser Lys Ser Lys Lys Leu Tyr Leu Ala Asp Asn Ala Phe Ser Gly
85 90 95

Leu Thr Val Pro Ser Met Glu Lys Ser Val Lys Ile Ser Thr Cys Val
100 105 110

Phe Ser Lys Gln Ile Leu Gly Pro Asn Ala Ser Thr Asn Ser Ser Asn
115 120 125

Ser Leu Val Val Arg Thr Ser Asn Glu Ala His Lys Phe Val Cys Phe
130 135 140

Ser Cys Met Ile Leu Asn Ser Leu Ala Ala Thr Gly Leu Gly
145 150 155

<210> 69
<211> 267
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 69

Met Ser Lys Ala Thr Tyr Lys Glu Arg Ala Ala Thr His Pro Ser Pro
1 5 10 15

Val Ala Ala Lys Leu Phe Asn Ile Met His Glu Lys Gln Thr Asn Leu
20 25 30

Cys Ala Ser Leu Asp Val Arg Thr Thr Lys Glu Leu Leu Glu Leu Val
35 40 45

Glu Ala Leu Gly Pro Lys Ile Cys Leu Leu Lys Thr His Val Asp Ile
50 55 60

Leu Thr Asp Phe Ser Met Glu Gly Thr Val Lys Pro Leu Lys Ala Leu
65 70 75 80

Ser Ala Lys Tyr Asn Phe Leu Leu Phe Glu Asp Arg Lys Phe Ala Asp
85 90 95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ala Gly Val Tyr Arg Ile
100 105 110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Val Gly Pro Gly
115 120 125

Ile Val Ser Gly Leu Lys Gln Ala Ala Glu Glu Val Thr Lys Glu Pro
130 135 140

Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Cys Lys Gly Ser Leu Ser
145 150 155 160

Thr Gly Glu Tyr Thr Lys Gly Thr Val Asp Ile Ala Lys Ser Asp Lys
165 170 175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Asp
180 185 190

Glu Gly Tyr Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
195 200 205

Lys Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Asp Asp Val Val
210 215 220

Ser Thr Gly Ser Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Ala Lys
225 230 235 240

Gly Arg Asp Ala Lys Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly Trp
245 250 255

Glu Ala Tyr Leu Arg Arg Cys Gly Gln Gln Asn
260 265

<210> 70
<211> 286
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 70

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
85 90 95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
100 105 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145 150 155 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
165 170 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
275 280 285